Phylogenetics beyond genes

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The concept of organisms being related in a way that can be depicted by an evolutionary tree was famously illustrated by Darwin, first in his notebooks and then in "*On the Origin of Species...*", where an evolutionary tree was the only figure. The concept was elaborated by Haeckel in the 1860s, and formed the basis of classification systems designed to reflect evolutionary relationships. The synthesis of the ideas of Mendelian genetics and Darwinian evolution, together with the subsequent availability of protein and nucleic acid sequence data, gave birth to the sequence-based phylogenetic analysis of the relationships between organisms. Such a phylogenetic analysis allows a number of features of the relationships among different groups to be inferred. How accurately can the data be modelled by a branching tree, rather than by some other kind of relationship? (This has been used as a test of evolutionary versus creationist theories.) What is the topology of the tree? (That is, which groups of organisms share common ancestry to the exclusion of others?) What are the branch lengths? (That is, how much change has taken place on particular lineages? Under certain assumptions, that information may be used to date the times of particular evolutionary divergences.)

Those attending this meeting will be familiar with the parallels between the copying of texts with the incorporation of changes and the error-prone replication of DNA, and the application of phylogenetic methodology to textual analysis. However, a number of other systems have been analysed in a similar way. We review some of them here.

Human organizations
A number of studies have attempted cladistic (therefore founded on evolutionary principles) analyses of manufacturing organizations. For example, McCarthy *et al.* have classified automotive manufacturing organizations in this way, allowing their identification as "agile producers", "lean producers", "just in time systems" and so on. This may have practical applications in allowing organizations to plan strategic change.

Cultural artefacts
The wide range of artefacts studied using phylogenetic methods includes pottery designs, arrowheads, musical instruments and woven textiles. Often, an important question here has been to determine how well characters can be described by a tree-like evolutionary pattern, or whether other patterns are more appropriate, indicating transfer among different cultural groups. We will look at examples involving Iranian textiles, the Baltic psaltery (a stringed instrument), and valved cornets.

Languages
Some of the most sophisticated phylogenetic analyses outside conventional biological sequence data have been carried out with languages. In this case, data come from comparisons of 'Swadesh lists' comprising words that have counterparts in most, if not all, languages. These include common verbs and nouns for body parts. Consideration

of whether a given word is effectively the same in two languages, such as 'water' in English or 'Wasser' in German, or different, such as 'eau' in French, provides the data for phylogenetic tree-building. The results have been used to provide insights into the relationships between different languages (tree topology). In addition, by calibrating the trees with known times of divergence of particular languages, the divergence times of other languages have been estimated. This in turn has allowed different archaeological models to be tested. The studies have also allowed features of language evolution, such as word half-lives, to be estimated.

We end by inviting discussion on other areas where phylogenetic analysis could be applied.